

Figure 1

1	GCTGAACAGACAAGAAATCACTTGAATGCTGGGGACATCACCTACTCTGTCCGGGCCATG	60
1	AlaGluGlnThrArgAsnHisLeuAsnAlaGlyAspIleThrTyrSerValArgAlaMet	20
61	GACCAGCTGGTAGGCCTCCTAGATGTACAGCTTCGGAACCTTGACCCAGGTGGAAAAGAT	120
21	AspGlnLeuValGlyLeuLeuAspValGlnLeuArgAsnLeuThrProGlyGlyLysAsp	40
121	AGTGCTGCCCCGAGTTTGAACAAGGCAATGGTCGAGACAGTTAACAACCTCCTTCAGCCA	180
41	SerAlaAlaArgSerLeuAsnLysAlaMetValGluThrValAsnAsnLeuLeuGlnPro	60
181	CAAGCTTTGAATGCATGGAGAGACCTGACTACGAGTGATCAGCTGCGTGGGCCACCATG	240
61	GlnAlaLeuAsnAlaTrpArgAspLeuThrThrSerAspGlnLeuArgAlaAlaThrMet	80
241	TTGCTTCATACTGTGGAGGAAAGTGCTTTTGTGCTGGCTGATAACCTTTTGAAGACTGAC	300
81	LeuLeuHisThrValGluGluSerAlaPheValLeuAlaAspAsnLeuLeuLysThrAsp	100
301	ATTGTCAGGGAGAATACAGACAATATTAAATTGGAAGTTGCAAGACTGAGCACAGAAGGA	360
101	IleValArgGluAsnThrAspAsnIleLysLeuGluValAlaArgLeuSerThrGluGly	120
361	AACTTAGAAGACCTAAAAATTTCCAGAAAACATGGGCCATGGAAGCACTATCCAGCTGTCT	420
121	AsnLeuGluAspLeuLysPheProGluAsnMetGlyHisGlySerThrIleGlnLeuSer	140
421	GCAAAATACCTTAAAGCAAAATGGCCGAAATGGAGAGATCAGAGTGGCCTTTGTCTGTAT	480
141	AlaAsnThrLeuLysGlnAsnGlyArgAsnGlyGluIleArgValAlaPheValLeuTyr	160
481	AACAACCTGGGTCTTATTATCCACGGAGAATGCCAGTATGAAGTTGGGAACGGAAGCT	540
161	AsnAsnLeuGlyProTyrLeuSerThrGluAsnAlaSerMetLysLeuGlyThrGluAla	180
541	TTGTCCACAAATCATCTCTGTATTGTCAATTCCCTGTTATTACGGCAGCAATAACAAA	600
181	LeuSerThrAsnHisSerValIleValAsnSerProValIleThrAlaAlaIleAsnLys	200
601	GAGTTTCAGTAACAAGGTTTATTTGGCTGATCCTGTGGTATTTACTGTTAAACATATCAAG	660
201	GluPheSerAsnLysValTyrLeuAlaAspProValValPheThrValLysHisIleLys	220
661	CAGTCAGAGGAAAATTTCAACCCTAACTGTTTCATTTTGGAGCTACTCCAAGCGTACAATG	720
221	GlnSerGluGluAsnPheAsnProAsnCysSerPheTrpSerTyrSerLysArgThrMet	240
721	ACAGGTTATTGGTCAACACAAGGCTGTGGCTCCTGACAACAAATAAGACACATACTACA	780
241	ThrGlyTyrTrpSerThrGlnGlyCysArgLeuLeuThrThrAsnLysThrHisThrThr	260
781	TGCTCTTGTAACCACCTAACAAATTTTGCAGTACTGATGGCAGTGTGGAAGTTAAGCAC	840
261	CysSerCysAsnHisLeuThrAsnPheAlaValLeuMetAlaHisValGluValLysHis	280
841	AGTGATGCGGTCCATGACCTCCTTCTGGATGTGATCAGCTGGGTGGAATTTTGCTGTCC	900
281	SerAspAlaValHisAspLeuLeuLeuAspValIleThrTrpValGlyIleLeuLeuSer	300
901	CTTGTTTGTCTCTCTGATTTGCATCTTCACATTTTGCTTTTCCGCGGGCTCCAGAGTGAC	960
301	LeuValCysLeuLeuIleCysIlePheThrPheCysPhePheArgGlyLeuGlnSerAsp	320
961	CGTAACACCATCCACAGAACCCTCTGCATCAGTCTCTTTGTAGCAGAGCTGCTCTTCCTG	1020
321	ArgAsnThrIleHisLysAsnLeuCysIleSerLeuPheValAlaGluLeuLeuPheLeu	340
1021	ATTGGGATCAACCGAAGTACCAACCAATTGCCGTGTGCTGTTTTCGCTGCCCTGTTACAT	1080
341	IleGlyIleAsnArgThrAspGlnProIleAlaCysAlaValPheAlaAlaLeuLeuHis	360
1081	TTCTTCTTCTTGGCTGCCCTTACCTGGATGTTCTCGAGGGGTGCAGCTTTATATCATG	1140
361	PhePhePheLeuAlaAlaPheThrTrpMetPheLeuGluGlyValGlnLeuTyrIleMet	380
1141	CTGGTGGAGGTTTTTGGAGGTGAACATTCACGTAGGAAATACTTTTATCTGGTCCGCTAT	1200
381	LeuValGluValPheGluSerGluHisSerArgArgLysTyrPheTyrLeuValGlyTyr	400
1201	GGGATGCCCTGCACTCATTGTGGCTGTGTACCTGCAGTAGACTACAGGAGTTATGGAACA	1260
401	GlyMetProAlaLeuIleValAlaValSerAlaAlaValAspTyrArgSerTyrGlyThr	420
1261	GATAAAGTATGTTGGCTCCGACTTGACACCTACTTCATTTGGAGTTTTATAGGACCAGCA	1320
421	AspLysValCysTrpLeuArgLeuAspThrTyrPheIleTrpSerPheIleGlyProAla	440
1321	ACTTTGATAATTATGCTTAATGTAATCTTCCTTGGGATTGCTTTATATAAAATGTTTCAT	1380
441	ThrLeuIleIleMetLeuAsnValIlePheLeuGlyIleAlaLeuTyrLysMetPheHis	460
1381	CATACTGCTATACTGAAACCTGAATCAGGCTGCTCTTGATAACATCAAGTCATGGGTATA	1440
461	HisThrAlaIleLeuLysProGluSerGlyCysLeuAspAsnIleLysSerTrpValIle	480
1441	GGTGCAATAGCTCTTCTCTGCCCTATTAGGATTGACCTGGGCCCTTGGACTCATGTATATT	1500
481	GlyAlaIleAlaLeuLeuCysLeuLeuGlyLeuThrTrpAlaPheGlyLeuMetTyrIle	500

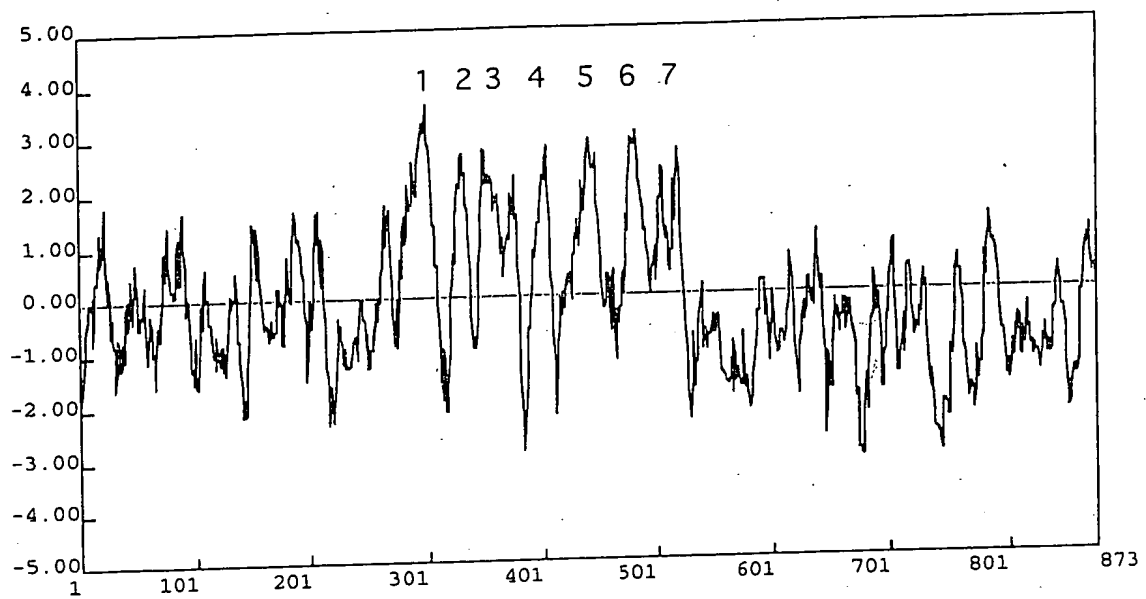
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Figure 2

1501 AATGAAAGCACAGTCATCATGGCCTATCTCTTACCATTTCATTTCTCTACAGGGAATG 1560  
 501 AsnGluSerThrValIleMetAlaTyrLeuPheThrIlePheAsnSerLeuGlnGlyMet 520  
 1561 TTTATATTTATTTTCCATTGTGTCTACAGAAGAAGGTACGAAAAGAGTATGGGAAATGC 1620  
 521 PheIlePheIlePheHisCysValLeuGlnLysLysValArgLysGluTyrGlyLysCys 540  
 1621 CTGCGAACACATTGCTGTAGTGGCAAAAGTACAGAGAGTTCCATTGGTTCAGGGAAAACA 1680  
 541 LeuArgThrHisCysCysSerGlyLysSerThrGluSerSerIleGlySerGlyLysThr 560  
 1681 TCTGGTTCTCGAACTCCTGGACGCTACTCCACAGGCTCACAGAGCCGAATCCGTAGAATG 1740  
 561 SerGlySerArgThrProGlyArgTyrSerThrGlySerGlnSerArgIleArgArgMet 580  
 1741 TGAATGACACGGTTCGAAAGCAGTCAGAGTCTTCCTTTTATTACTGGAGACATAAACAGT 1800  
 581 TrpAsnAspThrValArgLysGlnSerGluSerSerPheIleThrGlyAspIleAsnSer 600  
 1801 TCAGCGTCACTCAACAGAGAGGGGCTTCTGAACAATGCCAGGGATACAAGTGTCTATGGAT 1860  
 601 SerAlaSerLeuAsnArgGluGlyLeuLeuAsnAsnAlaArgAspThrSerValMetAsp 620  
 1861 ACTCTACCACTGAATGGTAACCATGGCAATAGTTACAGCATTGCCAGCGCGAATACCTG 1920  
 621 ThrLeuProLeuAsnGlyAsnHisGlyAsnSerTyrSerIleAlaSerGlyGluTyrLeu 640  
 1921 AGCAACTGTGTGCAATCATAGACCGTGGCTATAACCATAACGAGACCGCCCTAGAGAAA 1980  
 641 SerAsnCysValGlnIleIleAspArgGlyTyrAsnHisAsnGluThrAlaLeuGluLys 660  
 1981 AAGATTCTGAAGGAATCACTTCCAATATATCCCTTCTTACCTGAACAACCATGAGCGC 2040  
 661 LysIleLeuLysGluLeuThrSerAsnTyrIleProSerTyrLeuAsnAsnHisGluArg 680  
 2041 TCCAGTGAACAGAACAGGAATCTGATGAACAAGCTGGTGAATAACCTTGGCAGTGGAGG 2100  
 681 SerSerGluGlnAsnArgAsnLeuMetAsnLysLeuValAsnAsnLeuGlySerGlyArg 700  
 2101 GAAGATGATGCCATTGTCTGGATGATGCCACCTCGTTTAACCACGAGGAGAGTTTGGGC 2160  
 701 GluAspAspAlaIleValLeuAspAspAlaThrSerPheAsnHisGluGluSerLeuGly 720  
 2161 CTGGAACCTCATTATGAGGAATCTGATGCTCTCTTGTGCCCCAAGAGTATACTCCACC 2220  
 721 LeuGluLeuIleHisGluGluSerAspAlaProLeuLeuProProArgValTyrSerThr 740  
 2221 GAGAACCACAGCCACACCAATTATACCAGAAGGCGGATCCCCAAGACCACAGTGAGAGC 2280  
 741 GluAsnHisGlnProHisHisTyrThrArgArgIleProGlnAspHisSerGluSer 760  
 2281 TTTTTCCTTTTGCTAACCAACGAGCACACAGAAGATCTCCAGTCACCCCATAGAGACTCT 2340  
 761 PhePheProLeuLeuThrAsnGluHisThrGluAspLeuGlnSerProHisArgAspSer 780  
 2341 CTCTATACCAGCATGCCGACACTGGCTGGTGTGGCCGCCACAGAGAGTGTACCACCAGC 2400  
 781 LeuTyrThrSerMetProThrLeuAlaGlyValAlaAlaThrGluSerValThrThrSer 800  
 2401 ACCCAGACCGAACCCCCACCGCCAAATGTGGTGTATGCCGAAGATGTTTACTACAAAAGC 2460  
 801 ThrGlnThrGluProProProAlaLysCysGlyAspAlaGluAspValTyrTyrLysSer 820  
 2461 ATGCCAAACCTAGGCTCCAGAAACCAAGTCCATCAGCTGCATACTTACTACCAGTAGGT 2520  
 821 MetProAsnLeuGlySerArgAsnHisValHisGlnLeuHisThrTyrTyrGlnLeuGly 840  
 2521 CGCGGCAGCAGTGTATGATTTATAGTTCTTCCAAACAAAGATGGGACCCCTCCCGAGGGA 2580  
 841 ArgGlySerSerAspGlyPheIleValProProAsnLysAspGlyThrProProGluGly 860  
 2581 AGTTCAAAAGGACCGGCTCATTGGTCACTAGTCTATAGAAGATGACACAGAAATTGGAA 2640  
 861 SerSerLysGlyProAlaHisLeuValThrSerLeu\*\*\* 873  
 2641 CCAACAAAACCTGCTAACACCTTGTGACTGTTCTGAGTTGATATAAGCAGTGGTAATAAT 2700  
 873 873  
 2701 GTGTGTACTCCTAAATCTTTATGTGTCTCTTAAAGACAAACACAACTCTCAGACTTTT 2760  
 873 873  
 2761 TTTTTTTTTAATGGGATTTTGTAGTCCAGCCAGGGGAGAAAGATAACTGCTAAAAATCCC 2820  
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 2821 CTGTACCCGATCCTTTCTTGTCTTTCCCTTCAGATGGAGACTTCATTATGTTAATGAA 2880  
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 2941 ACATCTCTGATGCTGTGTTACTAAAATTACAAGGACCTGCTTTTTAAAGGCCAGAACA 3000  
 873 873

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Figure 3



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Figure 5

TOTAL " 324460

429	D	T	Y	F	I	W	S	F	I	G	P	A	T	L	I	I	M	L	N	V	I	F	L	G	I	A	L	Y	K	M	F	H	T	A	I	L	K	P	E	S	G	C	L	D	N	I	K	S	W	HK05006				
549	D	N	Y	F	I	W	S	F	I	G	P	V	T	F	I	I	L	L	N	I	I	F	I	V	I	T	L	C	K	M	V	K	H	S	N	T	L	K	P	D	S	S	R	L	E	N	I	K	S	W	HK05490			
479	V	I	G	A	I	A	L	L	C	L	L	G	L	T	W	A	F	G	L	M	Y	I	N	E	S	T	V	I	M	A	Y	L	F	T	I	F	N	S	L	Q	C	M	F	I	F	I	F	H	C	V	HK05006			
599	V	L	G	A	F	A	L	L	C	L	L	G	L	T	W	S	F	I	G	L	L	F	I	N	E	T	I	V	M	A	Y	L	F	T	I	F	N	A	F	Q	G	V	F	I	F	I	F	H	C	A	HK05490			
529	L	Q	K	K	V	R	K	E	Y	G	K	C	L	R	-	T	H	C	C	S	G	K	S	T	E	S	S	I	G	S	G	K	T	S	G	S	R	T	P	G	R	Y	S	T	G	S	Q	S	R	I	HK05006			
649	L	Q	K	K	V	R	K	E	Y	G	K	C	F	R	H	S	Y	C	C	G	G	L	P	T	E	S	P	H	S	S	V	K	A	S	T	T	R	T	S	A	R	Y	S	S	G	T	Q	S	R	I	HK05490			
578	R	R	N	W	N	D	T	V	R	K	Q	S	E	S	S	F	I	T	G	D	I	N	S	S	A	S	L	N	R	E	G	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	HK05006		
699	R	R	H	W	N	D	T	V	R	K	Q	S	E	S	S	F	I	S	G	D	I	N	S	T	S	T	L	N	-	Q	G	M	T	G	N	Y	L	L	T	N	P	L	L	R	P	H	G	T	N	N	HK05490			
610	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	HK05006			
748	P	Y	N	T	L	L	A	E	T	V	V	C	N	A	P	S	A	P	V	F	N	S	P	G	H	S	L	N	N	A	R	D	T	S	A	M	D	T	L	P	L	N	G	N	F	N	S	Y	S	HK05490				
634	I	A	S	G	E	Y	L	S	N	C	V	Q	I	I	D	R	G	Y	N	H	N	E	T	A	L	E	K	K	I	L	K	E	L	T	S	N	Y	I	P	S	Y	L	N	N	H	E	R	S	S	E	HK05006			
798	L	H	K	G	D	Y	-	N	D	S	V	Q	V	Y	D	C	G	L	S	L	N	D	T	A	F	E	K	M	I	I	S	E	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	HK05490	
684	C	N	R	N	L	M	N	K	L	V	N	N	-	-	L	G	S	G	R	E	D	D	A	I	V	L	D	D	A	T	S	F	N	H	E	E	S	L	G	L	E	L	I	H	E	E	S	D	A	P	HK05006			
839	K	T	H	N	L	E	L	T	I	P	V	K	P	V	I	G	G	S	S	S	E	D	D	A	I	V	A	D	A	S	S	L	M	H	S	D	N	P	G	L	E	L	H	H	K	K	E	L	E	A	P	HK05490		
732	L	L	P	P	R	V	Y	S	T	E	N	H	Q	P	H	H	Y	T	R	R	R	I	P	Q	D	H	S	E	S	F	F	P	L	L	T	N	E	H	T	E	D	L	Q	S	P	H	R	D	S	L	HK05006			
889	L	I	P	O	R	T	H	S	L	-	Y	Q	P	Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	HK05490			
782	Y	T	S	M	P	T	L	A	G	V	A	A	T	E	S	V	T	T	S	T	Q	T	E	P	P	P	A	K	C	G	D	A	E	D	V	Y	Y	K	S	M	P	N	L	G	S	R	N	H	V	H	HK05006			
934	Y	T	S	M	P	N	L	R	D	S	P	Y	P	E	S	-	S	P	D	M	E	E	D	L	S	P	S	R	R	S	E	N	E	D	I	Y	Y	K	S	M	P	N	L	G	A	-	-	-	-	-	-	-	-	HK05490
832	Q	L	H	T	Y	Y	Q	L	G	R	G	S	S	D	G	F	I	V	P	P	N	K	D	G	T	P	P	E	C	S	S	K	-	G	P	A	H	L	V	T	S	L	HK05006											
980	Q	L	C	N	C	Y	Q	I	S	R	G	N	S	D	G	Y	I	T	P	I	N	K	E	G	C	I	P	E	G	D	V	R	E	G	Q	M	Q	L	V	T	S	L	HK05490											

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Figure 6

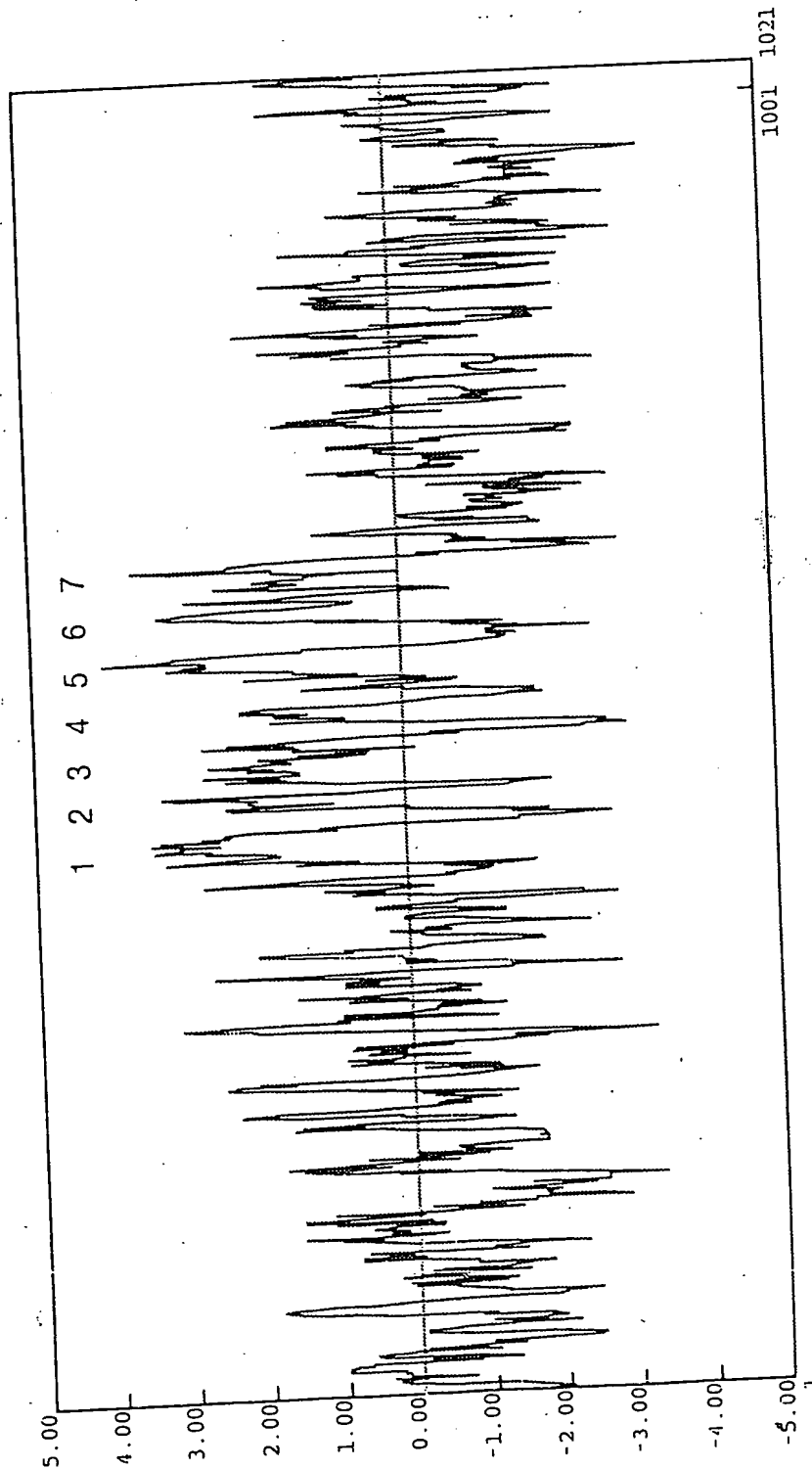


Figure 7

1	GAAGGAAGCAAGGACAAACACCTCCAGCAGTTTCTACCAACCAAAATTCACCTATA	60
1	GlUGlySerLysGlyThrLysProProAlaValSerThrThrLysIleProProIle	20
61	ACAAATATTTTCCCTCCAGAGAGATTCTGTGAAGCAATTAGACTCCAGGGGATAAAG	120
21	ThrAsnIlePheProLeuProGluArgPheCysGluAlaLeuAspSerLysGlyIleLys	40
121	TGGCCTCAGACACAAAGGGGAATGATGTTGAACGACCATGCCCTAAGGGAACAAGAGA	180
41	TrpProGlnThrGlnArgGlyMetMetValGluArgProCysProLysGlyThrArgGly	60
181	ACTGCCTCATATCTCTGCATGATTTCCACTGGAACATGGAACCTTAAGGGCCCCGATCTT	240
61	ThrAlaSerTyrLeuCysMetIleSerThrGlyThrTrpAsnProLysGlyProAspLeu	80
241	AGCAACTGTACCTCACACTGGTCAATCAGCTGGCTCAGAAGATCAGAAGCGGAGAAAAT	300
81	SerAsnCysThrSerHisTrpValAsnGlnLeuAlaGlnLysIleArgSerGlyGluAsn	100
301	GCTGCTAGTCTTGCCCAATGAAGTGGCTAAACATACCAAGGGCCAGTGTTCCTGGGAT	360
101	AlaAlaSerLeuAlaAsnGluLeuAlaLysHisThrLysGlyProValPheAlaGlyAsp	120
361	GTAAGTCTTCAGTGAGATTGATGGAGCAGTGGTGGACATCCTTGATGCCACAGCTGCAG	420
121	ValSerSerSerValArgLeuMetGlnGlnLeuValAspIleLeuAspAlaGlnLeuGln	140
421	GAAGTGAACCTAGTGAAAAGATTTCAGCTGGACGGAGTTATAACAGCTCCAAAACGA	480
141	GluLeuLysProSerGluLysAspSerAlaGlyArgSerTyrAsnLysLeuGlnLysArg	160

Figure 8

481 GAGAGACATGACGGGCTTACCTTAAGCAATTGTGACACAGTGGACAACCTTCTGAGA 540  
161 GluLysThrCysArgAlaTyrLeuLysAlaIleValAspThrValAspAsnLeuLeuArg 180

541 CCTGAAGCTTTGGAAATCATGGAACATATGAATTCCTTCTGAACAAGCACATACGCAACA 600  
181 ProGluAlaLeuGluSerTrpLysHisMetAsnSerSerGluGlnAlaHisThrAlaThr 200

601 ATGTTACTCGATACATGGAAGAGGAGCTTTGTCTAGCTGACAAATCTTTAGAACCA 660  
201 MetLeuLeuAspThrLeuGluGluGlyAlaPheValLeuAlaAspAsnLeuLeuGluPro 220

661 ACAAGGTCCTCAATGCCACAGAAATATTTGTCCTGGAGTTGCCGTACTCAGTACAGAA 720  
221 ThrArgValSerMetProThrGluAsnIleValLeuGluValAlaValLeuSerThrGlu 240

721 GGACAGATCCAAGACTTTAAATTTCTCTGGCATCAAGAGCAGGACGCTCAATCCAA 780  
241 GlyGlnIleGlnAspPheLysPheProLeuGlyIleLysGlyAlaGlySerSerIleGln 260

781 CTGTCCGCAATACCGTCAACAGAACAGCAGGAATGGGCTTGCNAAGTTGGTGTTCATC 840  
261 LeuSerAlaAsnThrValLysGlnAsnSerArgAsnGlyLeuAlaLysLeuValPheIle 280

841 ATTTACCGGAGCTGGACAGTTCTTGTAGTACAGAAATGCAACCATTAACCTGGTGCT 900  
281 IleTyrArgSerLeuGlyGlnPheLeuSerThrGluAsnAlaThrIleLysLeuGlyAla 300

901 GATTTTATTTGCTGTAATAGCACCATTTGCAGTGAACCTCAGTCAATTCAGTTTCAATC 960  
301 AspPheIleGlyArgAsnSerThrIleAlaValAsnSerHisValIleSerValSerIle 320

961 AATAAGAGTCCAGCCGAGTATACCTGACTGATCTGTGCTTTTACCCCTGCCACACATT 1020

Figure 9

321 AsnLysGluSerSerArgValTyrLeuThrAspProValLeuPheThrLeuProHisIle 340  
1021 GATCCTGACAATTATTTCAATGCAAACTGCTCTCTGGAACACTACACAGAGAACTATG 1080  
341 AspProAspAsnTyrPheAsnAlaAsnCysSerPheTrpAsnTyrSerGluArgThrMet 360  
1081 ATGGGATATTGCTCTACCCAGGGCTGCAAGCTGGTTGACACTAATAAACTCGAACACG 1140  
361 MetGlyTyrTrpSerThrGlnGlyCysLysLeuValAspThrAsnLysThrArgThrThr 380  
1141 TGTGCATGCAGCCACCTAACCAATTTTGGCAATCTCATGGCCACAGGAAATTCATAT 1200  
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1201 AAAGATGGCGTTCATGANTTACTTCTTACAGTCATCACCTGGGTGGAAATGTCTTTCC 1260  
401 LysAspGlyValHisGluLeuLeuLeuThrValIleThrTrpValGlyIleValIleSer 420  
1261 CTTGTTTCCCTGGCTATCTGCATCTTCACCTTCTGCTTTTCCGTTGGCCTACAGAGTGAC 1320  
421 LeuValCysLeuAlaIleCysIlePheThrPheCysPhePheArgGlyLeuGlnSerAsp 440  
1321 CGAAATACTATTACAGAAGAACCTTTTGTATCAACCTTTTCATGCTGAATTTTCTTA 1380  
441 ArgAsnThrIleHisLysAsnLeuCysIleAsnLeuPheIleAlaGluPheIlePheLeu 460  
1381 ATAGGCATTGATAAGACAAAATATGCGATTGCATGCCCAATATTTGCAGGACTTCTACAC 1440  
461 IleGlyIleAspLysThrLysTyrAlaIleAlaCysProIlePheAlaGlyLeuLeuHis 480

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Figure 10.

1441 TTTTCTTTTGGCAGCTTTTGCTTGGATGTGCTAGAAGGTGTGCAGCTCTACCTAATG 1500  
 481 PhePhePheLeuAlaAlaPheAlaTrpMetCysLeuGluGlyValGlnLeuTyrLeuMet 500  
 1501 TTAGTTGAAGTTTTTGAAAGTGAATATTCAAGGAAAAAATATTACTATGTTGCTGGTTAC 1560  
 501 LeuValGluValPheGluSerGluTyrSerArgLysLysTyrTyrTyrValAlaGlyTyr 520  
 1561 TTGTTTCTGCCACAGTGGTTGGAGTTTCAGCTGCTATTGACTATAAGAGCTATGGAACA 1620  
 521 LeuPheProAlaThrValValGlyValSerAlaAlaIleAspTyrLysSerTyrGlyThr 540  
 1621 GAAAAAGCTTGCTGGCTTCATGTTGATAACTACTTTATATGGAGCTTCATTGGACCTGTT 1680  
 541 GluLysAlaCysTrpLeuHisValAspAsnTyrPheIleTrpSerPheIleGlyProVal 560  
 1681 ACC TTCATTATTCTGCTAAATATTATCTTCTTGCTGATCACATTGTGCAAAATGGTGAAG 1740  
 561 ThrPheIleIleLeuLeuAsnIleIlePheLeuValIleThrLeuCysLysMetValLys 580  
 1741 CATTCAAACACTTTGAAACCAGATTCTAGCAGGTGGAACATTAAAGTCTTGGGTGCTT 1800  
 581 HisSerAsnThrLeuLysProAspSerSerArgLeuGluAsnIleLysSerTrpValLeu 600  
 1801 GGCGCTTTGCTCTTCTGTGTCTTCTTGGCCTCACCTGGTCCTTTGGGTGCTTTTTATT 1860  
 601 GlyAlaPheAlaLeuLeuCysLeuLeuGlyLeuThrTrpSerPheGlyLeuLeuPheIle 620  
 1861 AATGAGGAGACTATTGTGATGGCATATCTCTTCACTATATTTAATGCTTTCCAGGGAGTG 1920  
 621 AsnGlnGluThrIleValMetAlaTyrLeuPheThrIlePheAsnAlaPheGlnGlyVal 640  
 1921 TTCATTTTCATCTTTCACTGTGCTCTCCAAAAGAAAGTACGAAAAGATATGGCAAGTGC 1980  
 641 PheIlePheIlePheHisCysAlaLeuGlnLysLysValArgLysGluTyrGlyLysCys 660

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Figure 11

1981 TTCAGACATCATCTGCTGTGGAGGCTCCCAACTGAGAGTCCCCACAGTTCAGTGAAG 2040  
 661 PheArgHisSerTyrCysGlyGlyLeuProThrGluSerProHisSerSerVallys 680  
 2041 GCATCAACCAACAGAACCCAGTGTCTGGCTATTCTCTCTGGCACACAGAGTCGTATAAGAAGA 2100  
 681 AlaSerThrThrArgThrSerAlaArgTyrSerSerGlyThrGlnSerArgIleArgArg 700  
 2101 ATGTGGNAATGATCTGTGAGAAACAATCAGATCTCTCTTTTATCTCAGGTGACATCAAT 2160  
 701 MetTrpAsnAspThrValArgLysGlnSerGluSerSerPheIleSerGlyAspIleAsn 720  
 2161 AGCACTTCAACACTTAATCAAGGAATGAGTGGCAATTACCTACTAACAACCCCTCTTCTT 2220  
 721 SerThrSerThrLeuAsnGlnGlyMetThrGlyAsnTyrLeuLeuThrAsnProLeuLeu 740  
 2221 CGACCCCAAGGCACTAACAACCCCTATATACACATGCTCGCTGGAACAGTGTGTATGTAAT 2280  
 741 ArgProHisGlyThrAsnAsnProTyrAsnThrLeuLeuAlaGluThrValValCysAsn 760  
 2281 GCCCCCTCAGCTCCGTATTTAACTCACCAGGACATTCATCGAACAAATGCCAGGGATACA 2340  
 761 AlaProSerAlaProValPheAsnSerProGlyHisSerLeuAsnAsnAlaArgAspThr 780  
 2341 AGTGCCATGGATCTCTACCGCTAAATGGTAATTTTAAACACAGCTACTCGCTGCACAAG 2400  
 781 SerAlaMetAspThrLeuProLeuAsnGlyAsnPheAsnAsnSerTyrSerLeuHisLys 800  
 2401 GGTGACTATAATGACAGCGGTGCAAGTTGTGGACTGTGGACTAAGTCTGAATGATAGTCT 2460  
 801 GlyAspTyrAsnAspSerValGlnValValAspCysGlyLeuSerLeuAsnAspThrAla 820

Figure 12

2461 TTGAGAAATGATCAATTCAGAATTAGTCACAACAACCTACGGGCGACGACAAGACT 2520  
821 PheGluLysMetIleIleSerGluLeuValHisAsnAsnLeuArgGlySerSerLysThr 840

2521 CACAACCTCGAGCTCAGGCTACCGCTACAGTCAACCTGTGATTGGAGGTAGCAGCAGTGAAGAT 2580  
841 HisAsnLeuGluLeuThrLeuProValLysProValIleGlyGlySerSerSerGluAsp 860

2581 GATGCTATTGTGGCAGATGCTTCATCTTTAATGCACAGCGACAACCCAGGGCTGGAGCTC 2640  
861 AspAlaIleValAlaAspAlaSerSerLeuMetHisSerAspAsnProGlyLeuGluLeu 880

2641 CATCACAAGAACTCGAGGCCACCTATTTCCTCAGCGGACTCACTCCCTTCGTACCAA 2700  
881 HisHisLysGluLeuGluAlaProLeuIleProGlnArgThrHisSerLeuLeuTyrGln 900

2701 CCCCAGAAAGTGAAGTCCGAGGGAACCTGACAGCTATGTCTCCCACTGACAGCAGAG 2760  
901 ProGlnLysLysValLysSerGluGlyThrAspSerTyrValSerGlnLeuThrAlaGlu 920

2761 GCTGAAGATCACTACAGTCCCCCAACAGAGACTCTCTTTATACAGCATGCCCAATCTT 2820  
921 AlaGluAspHisLeuGlnSerProAsnArgAspSerLeuTyrThrSerMetProAsnLeu 940

2821 AGAGACTCTCCCTATCCGGAGAGAGCCCTGACATGGAAGAAGACCTCTCTCCCTCCAGG 2880  
941 ArgAspSerProTyrProGluSerSerProAspMetGluGluAspLeuSerProSerArg 960

2881 AGGAGTGAGATGAGGACATTACTATATAAAGCANTGCCAATCTTGGAGCTGGCCATCAG 2940  
961 ArgSerGluAsnGluAspIleTyrTyrLysSerMetProAsnLeuGlyAlaGlyHisGln 980

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Figure 13

2941 CTTGAGATGTGCTACAGATCAGCAGGGCAATAGTATGTTATATAATCCCCATTAAAC 3000  
981 LeuGlnMetCysTyrGlnIleSerArgGlyAsnSerAspGlyTyrIleIleProIleAsn 1000

3001 AAAGAAGGGTGTATTCCAGAAGGAGATGTTAGAGAAGGACAAATGCCAGCTGTTACAAGT 3060  
1001 LysGluGlyCysIleProGluGlyAspValArgGluGlyGlnMetGlnLeuValThrSer 1020

3061 CTTTAATCATACAGCTAAGGANTTCCAAGGGCCACATGCCGAGTATTATAATAAAGACA 3120  
1021 Leu\*\*\* 1022

3121 CCAATGGCCTGACGCGAGCTCCCTCAAACTCTGCTTGAAGAGATGACTCTGACCTGTGGT 3180  
1022 1022

3181 TCTCTGGTGTAATAAAGATGACTGAACCTTGCAGTTCCTGTAATTTTATAAACAATACA 3240  
1022 1022

3241 AAAACTTTGTATATACACAGATGATCTAAAGTGAATTATTGTTACAAAGAAAGAGAT 3300  
1022 1022

3301 GCCAGCCAGGTATTTTAAGATTCTGCTGCTGTTTGAAGAAATGTGAACAAGCAAAACA 3360  
1022 1022

3361 AAACTTTCAGCCATTATTACTGCGCAGCTCTGTGAACTAAATTTGTAAATATGCGCTGCAC 3420  
1022 1022

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Figure 14

3421	CATTTTGTAGGCCTGCTTGTATTATATACAAGACGTAGGCTTAAATCCGTGGGAC	3480
1022		1022
3481	AAATTTACTGTACCTTACTATTCCCTGACAGACTGGAAAGCAGAGAGATATTCTGCA	3540
1022		1022
3541	TCAGTTGCAGTTCACTGCAANTCTTTTACATTNAGGCAANGATTGAAACATGCTTAAC	3600
1022		1022
3601	CACTAGCAATCAAGCCACAGGCCCTTATTTCATATGTTTCTCAACTGTACATGAACCTAT	3660
1022		1022
3661	TCTCATGAAATAAGCGCTAAGAAATATATTTTTGTCTATTGCTAGGGTAAATAAATAC	3720
1022		1022
3721	ATTGTGTCCAACTGAAATATAATGTTCATTAAATAATTTTAAAGAGTGAAGAAATAT	3780
1022		1022
3781	TGTGAAAGCTCTGTGGTNGCACATGTTATGAANGTTTTTCTTACACTTTGTCTATGGTA	3840
1022		1022
3841	AGTTCTACTCATTTTCACTTCTTTTCCACGTATATACAGTGTCTGTCTTTGACAAAGTTAG	3900
1022		1022
3901	TCTTTTATTACTTACATTTAAATTTCTTTATTTGCCAAAGAACGTTGTTTATGGGAGAAAC	3960

Figure 15

1022  
1022  
3961 AAACCTCTTTGAAGCCAGTTAAGTCATCCCTTGACAAAGTGAAGAATCTAGAAAAGAT 4020  
1022  
4021 TGTGTGTCACCCCTGTTTATTCTTGAACAGAGGGCAAGAGGGCACATGGGCACCTTCTCAC 4080  
1022  
4081 AAACCTCTTCTAGTGAACAAAAGGTGCCCTATTCTTTTAAAAAATAAATAAACATAAA 4140  
1022  
4141 TATTACTCTTCCATANTCCCTTCGCTATATTCTAGTAATTAAATTATTTATGATAAAGT 4200  
1022  
4201 TCTAATGAANTGTAAATGTGTTTCAGCAAAATCTGCTTTTTTTTTCATCCCTTTGTTGTA 4260  
1022  
4261 CCTGTAAATAATGAGGCCCATCACTAATATCCAGTGTAAAGTTTAAACACGGTTTGACAGTA 4320  
1022  
4321 AATAAATGTGAATTTTTCAGT 4343  
1022

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Figure 16

	1				50
HK05006					
HK05490					
HH02631	MARLA AVLWN	LCVTAVLVTS	ATQGLSRAGL	PFGLMRRELA	CEGYPIELRC
	51				100
HK05006					
HK05490					
HH02631	PGSDVIMVEN	ANYGRTDDKI	CDADPFQMEN	VQCYLPDAFK	IMSQR CNNRT
	101				150
HK05006					
HK05490					
HH02631	QCVVVAGSDA	FPDPCPGTYK	YLEVQYDCVP	YKVEQKV FVC	PGTLQKVLEP
	151				200
HK05006					
HK05490					
HH02631	TSTHESEHQS	GAWCKDPLQA	GDRIYVMPWI	PYRTDTL TEY	ASWEDYVAAR
	201				250
HK05006					
HK05490					
HH02631	HTTTYRLPNR	VDGTGFVVYD	GAVFYNKERT	RNIVKYDLRT	RIKSGETVIN
	251				300
HK05006					
HK05490					
HH02631	TANYHDTSPY	RWGGKTDIDL	AVDENGLWVI	YATEGNNGRL	VVSQ LNPYTL
	301				350
HK05006					
HK05490					
HH02631	RFEGTWETGY	DKRSASNAFM	VCGVLYVLRS	VYVDDDSEAA	GNRV DYAFNT

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Figure 17

	351				400
HK05006					
HK05490					
HH02631	NANREEPVSL	TFPNPYQFIS	SVDYNPRDNQ	LYVWNNYFVV	RYSLEFGPPD
	401				450
HK05006					
HK05490					E
HH02631	PSAGPATSP	LSTTTTARPT	PLTSTASPAA	TTPLRRAPLT	THPVGAINQL
	451				500
HK05006					
HK05490	GSKGTPPPA	VSTTKIPPIT	NIFPLPERFC	EALDSKGIKW	PQTQRGMMVE
HH02631	GPLPAPATAP	VPSTRRPPAP	NLHVSPFLFC	EPREVRVQW	PATQQGMLVE
	501				550
HK05006					
HK05490	RPCPKGTRGT	ASYLCMISTG	TWNPKGPDLS	NCTSHWVNQL	AQKIRSGENA
HH02631	RPCPKGTRGI	ASFQCLPALG	LWNPRGPDLS	NCTSPWVNQV	AQKIKSGENA
	551				600
HK05006	AEQ	TRNHLNAGDI	TYSVRAMDQL	VGLLDVQLRN	LTPGGKDSAA
HK05490	ASLANELAKH	TKGPVFAGDV	SSSVRLMEQL	VDILDAQLQE	LKPSEKDSAG
HH02631	ANIASELARH	TRGSIYAGDV	SSSVKLMEQL	LDILDAQLQA	LRPIERESAG
	601				650
HK05006	RSLN. ....	..... KAM	VETVNNLLQP	QALNAWRDLT	TSDQLRAATM
HK05490	RSYNKLQKRE	KTCRAYLKAI	VDTVNDLLRP	EALSWKHMN	SSEQAHTATM
HH02631	KNYNKMHKRE	RTCKDYIKAV	VETVDNLLRP	EALSWKDMN	ATEQVHTATM
	651				700
HK05006	LLHTVEESAF	VLADNLLKTD	IVRENTDNIK	LEVARLSTEG	NLEDLKFP. E
HK05490	LLDTLEEGAF	VLADNLLIPT	RVSMTPTENIV	LEVAVLSTEG	QIQDFKFLPG
HH02631	LLDVLEEGAF	LLADNVREPA	RFLAAKENVV	LEVTVLNTEG	QVQELVFPQE

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Figure 18

	701		750
HK05006	NMGHGSTIQL	SANTLKQNGR	NGEIRVAFVL YNNLGPYLST ENASMKLGTE
HK05490	IKGAGSSIQL	SANTVKQNSR	NGLAKLVFII YRSLGQFLST ENATIKLGAD
HH02631	EYPRKNSIQL	SAKTIKQNSR	NGVVKVVFIL YNNLGLFLST ENATVKLAGE
	751		800
HK05006	A...LSTNHS	VIVNSPVITA	AINKEFSNKV YLADPVVFTV KHIKQSEENF
HK05490	F...IGRNST	IAVNSHVISV	SINKE. SSRV YLTDPVLFTL PHI. DPDNYF
HH02631	AGPGGPGGAS	LVVNSQVIAA	SINKE. SSRV FLMDPVIFTV AHL. EDKNHF
	801		850
HK05006	NPNCSEFWSYS	KRTMTGYWST	QGCRLTTNK THHTCSCNHL TNFAVLMAHV
HK05490	NANCSFWNYS	ERTMMGYWST	QGCKLVDTNK TRTTCACSHL TNFAILMAHR
HH02631	NANCSFWNYS	ERSMLGYWST	QGCRLVESNK THHTCACSHL TNFAVLMAHR
	851		900
HK05006	EVKHSDAVHD	LLLDVITWVG	ILLSLVCLLI CIFTFCFFRG LQSDRNTIHK
HK05490	EIAYKDGVE	LLLTVITWVG	IVISLVCLAI CIFTFCFFRG LQSDRNTIHK
HH02631	EI. YQGRINE	LLLSVITWVG	IVISLVCLAI CISTFCFLRG LQTDNRNTIHK
	901		950
HK05006	NLCISLFVAE	LLFLIGINRT	DQPIACAVFA ALLHFFFLAA FTWMFLEGVQ
HK05490	NLCINLFIAE	FIFLIGIDKT	KYAIACPIFA GLLHFFFLAA FAWMCLEGVQ
HH02631	NLCINLFLAE	LLFLVGIDKT	QYEIACPIFA GLLHYFFFLAA FSWLCLEGVH
	951		1000
HK05006	LYIMLVEVFE	SEHSRRKYFY	LVGYGMPALI VAVSAAVDYR SYGTDKVCWL
HK05490	LYLMLVEVFE	SEYSRKKYYY	VAGYLFPATV VGVSAAIDYK SYGTEKACWL
HH02631	LYLLLVEVFE	SEYSRTKYYY	LGGYCFPALV VGIAAAIDYR SYGTEKACWL
	1001		1050
HK05006	RLDTYFIWSF	IGPATLIIML	NVIFLGIALY KMFHHTAILK PESGCLDNIK
HK05490	HVDNYFIWSF	IGPVTFIILL	NIIFLVITLC KMKVHSNTLK PDSSRLENIK
HH02631	RVDNYFIWSF	IGPVSVFIVV	NLVFLMVT LH KMIRSSSVLK PDSSRLDNIK

FOI b7E b7C b7D b7F b7G b7H b7I b7J b7K b7L b7M b7N b7O b7P b7Q b7R b7S b7T b7U b7V b7W b7X b7Y b7Z

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Figure 19

	1051	1100
HK05006	SWVIGAIALL CLLGLTWAFG LMYINESTVI MAYLFTIFNS LQGMFIFIFH	
HK05490	SWVLGAFALL CLLGLTWSFG LLFINEETIV MAYLFTIFNA FQGVFIFIFH	
HH02631	SWALGAIALL FLLGLTWAFG LLFINKESVV MAYLFTTFNA FQGVFIFVFH	
	1101	1150
HK05006	CVLQKKVRKE YGKCLR. THC CSGKSTESSI GSGKTSGSRT PGRYSTGSQS	
HK05490	CALQKKVRKE YGKCFRHSYC CGGLPTESPH SSVKASTTRT SARYSSGTQS	
HH02631	CALQKKVHKE YSKCLRHSYC CIRSPPGGTH GSLKTSAMRS NTRYTGTQS	
	1151	1200
HK05006	RIRRMWNDTV RKQSESSFIT GDINSSASLN REGLLN. ....	
HK05490	RIRRMWNDTV RKQSESSFIS GDINSTSTLN QGMTGNYLLT NPLLPHGTN	
HH02631	RIRRMWNDTV RKQTESSFMA GDINSTPTLN RGTMGNHLLT NPVLQPRGGT	
	1201	1250
HK05006	..... NARDTS VMDTLPLNGN	
HK05490	NPYNTLLAET VVCNAPSAPV FNSPGHSLN. .... NARDTS AMDTLPLNGN	
HH02631	SPYNTLIAES VGFNPSSPPV FNSPGSYREP KHPLGGREAC GMDTLPLNGN	
	1251	1300
HK05006	HGNSYSIASG EYLSN. CVQI IDRGYNHNE. TALEKKILKE LTSNYIPSYL	
HK05490	FNNSYSLHKG DY. . NDSVQV VDCGLSLND. TAFEKMIISE LVHN. ... NL	
HH02631	FNNSYSLRSG DFPPGDDGPE PPRGRNLADA AAFEKMIISE LVHN. ... NL	
	1301	1350
HK05006	NNHERSSEQN RNLMNKL VNN LGSGREDDAI VLDDATSFNH EESLGLELIH	
HK05490	RGSSKTHN. . LELTLPVKPV IGGSSSEDDA IVADASSLMH SDNPGLELHH	
HH02631	RGSSSAAKGP PPPEPPVPPV PGGGGEE. ... EAGGPGG ADRAEIELLY	
	1351	1400
HK05006	EESDAPLLPP RYVSTENHQP HHYTRRRIPQ DHSSEFFPLL TNEHTEDLQS	
HK05490	KELEAPLIPQ RTHSL. .... LYQPQKKVKS EGTDSYVSQ L TAEADHLQS	
HH02631	KALEEPLLLP RAQSV. .... LYQSD. ... L DESECTAED GATSRPLSSP	

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Figure 20

1401 1450  
HK05006 PHRDSLYTSM PTLAGVAATE SVTTSTQTE. . . PPPAKCGD AEDVYYKSM.  
HK05490 PNRDSLYTSM PNLRDSP. YP ESSPDMEEDL . . . SPSRRSE NEDIYYKSM.  
HH02631 PGRDSLYASG ANLRDSPSYP DSSPEGPSEA LPPPPPAPPG PPEIYYTSRP

1451 1500  
HK05006 PNLGSRNHVH QLHTYYQLGR GSSDGFIVPP NKDGTPEGS . SKGPAHLVT  
HK05490 PNLGAG. . . H QLQMCYQISR GNSDGYIPI NKEGCIPEGD VREGQMLVT  
HH02631 PALVAR. . . N PLQGYQVRR PSHEGYLAAP GLEGPGPDGD . . . GQMQLVT

1501  
HK05006 SL  
HK05490 SL  
HH02631 SL

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Figure 21

TTTTTTTTTTTTTTTTTTCTAATTTTTGGTCGGCGGCGGTGCTGGGCCAG 50  
 GGGAAGGAAGGGACACGGAGGCCGCCCTCGTCCCGCCACCTCCTACCCGC 100  
 TTCCCCCAGCCCCGGCTCCGGGAGATGTGCCGGGCGGGGGGCCCGGGTT 150  
 CGCCGAGCCGCAGGAGAGACACGCTGGGCCGACCCCAGAGAGGCGCTGGA 200  
 CAGGCTGGTGGTCCAGGCCGTGGTGCCTGCCAGGTGATGTGGGGCAAAGC 250  
 CCCCCGCACAGGCCACTGAGAGCTCCGGACACGCACCCGGCTGCCACCAT 300  
 GGCCCGCCTAGCCGCAGTGCTCTGGAATCTGTGTGTACCCGCCGTCTTG 350  
 TCACCTCGGCCACCCAAGGCCTGAGCCGGGCGGGCTCCCGTTCGGGCTG 400  
 ATGCGCCGGGAGCTGGCGTGTGAAGGCTACCCCATCGAGCTGCGGTGCC 450  
 CGGCAGCGACGTCATCATGGTGGAGAATGCCAACTACGGGCGCACGGACG 500  
 ACAAGATTTGCGATGCTGACCCTTTCCAGATGGAGAATGTGCAGTGCTAC 550  
 CTGCCGGACGCCTTCAAGATCATGTACAGAGGTGTAACAACCGCACCCA 600  
 GTGCGTGGTGGTCCCGGCTCGGATGCCTTTCTTGACCCCTGTCCTGGGA 650  
 CCTACAAGTACCTGGAGGTGCAGTACGACTGTGTCCCCTACAAAGTGGAG 700  
 CAGAAAGTCTTCGTGTGCCAGGGACCCTGCAGAAGGTGCTGGAGCCAC 750  
 CTCGACACACGAGTCAGAGCACCACTGTGGCGCATGGTGCAAGGACCCGC 800  
 TGCAGGCGGGTGACCGCATCTACGTGATGCCCTGGATCCCCTACCGCACG 850  
 GACACACTGACTGAGTATGCCTCGTGGGAGGACTACGTGGCCGCCCGCCA 900  
 CACCACCACCTACCGCCTGCCCAACCGCGTGGATGGCACAGGCTTTGTGG 950  
 TCTACGATGGTGCCGTCTTCTACAACAAGGAGCGCACGCGCAACATCGTC 1000  
 AAGTATGACCTACGGACGCGCATCAAGAGCGGGGAGACGGTCATCAATAC 1050  
 CGCCAACCTACCATGACACCTCGCCCTACCGCTGGGGCGGAAAGACCGACA 1100  
 TTGACCTGGCGGTGGACGAGAACGGGCTGTGGGTCTATCTACGCCACTGAG 1150  
 GGCAACAACGGGCGGCTGGTGGTGAGCCAGCTGAACCCCTACACACTGCG 1200  
 CTTTGAGGGCACGTGGGAGACGGGTTACGACAAGCGCTCGGCATCCAACG 1250  
 CCTTCATGGTGTGTGGGGTCTGTACGTCCTGCGCTCCGTGTACGTGGAT 1300  
 GATGACAGCGAGGCGGCTGGCAACCGCGTGGACTATGCCTTCAACACCAA 1350  
 TGCCAACCGCGAGGAGCCTGTCAGCCTCACCTTCCCCAACCCCTACCACT 1400  
 TCATCTCCTCCGTTGACTACAACCCTCGCGACAACCAGCTGTACGTCTGG 1450  
 AACAACTATTTTCGTGGTGGCTACAGCCTGGAGTTCGGGCGGCCGACCC 1500  
 CAGTGCTGGGCCAGCCACTTCCCCACCCCTCAGCACGACCACCACAGCCA 1550  
 GGCCACGCCCCCTCACCAGCACAGCCTCGCCCGCAGCCACCACCCCGCTC 1600  
 CGCCGGGCACCCCTCACCAGCACACCCAGTGGGTGCCATCAACCAGCTGGG 1650  
 ACCTGATCTGCCTCCAGCCACAGCCCCAGTCCCCAGCACCCGGCGGCCCC 1700  
 CAGCCCCGAATCTACACGTGTCCCTGAGCTCTTCTGCGAGCCCCGAGAG 1750

Figure 22

GTACGGCGGGTCCAGTGGCCGGCCACCCAGCAGGGCATGCTGGTGGAGAG 1800  
GCCCTGCCCAAGGGGACTCGAGGAATTGCCTCCTTCCAGTGTCTACCAG 1850  
CCTTGGGGCTCTGGAACCCCCGGGGCCCTGACCTCAGCAACTGCACCTCC 1900  
CCCTGGGTCAACCAGGTGGCCAGAGATCAAGAGTGGGGAGAACGCGGC 1950  
CAACATCGCCAGCGAGCTGGCCCGACACACCCGGGGCTCCATCTACGCGG 2000  
GGGACGTCTCCTCCTCTGTGAAGCTGATGGAGCAGCTGCTGGACATCCTG 2050  
GATGCCCAGCTGCAGGCCCTGCGGCCCATCGAGCGGAGTCAGCCGGCAA 2100  
GAACTACAACAAGATGCACAAGCGAGAGAGAACTTGTAAGGATTATATCA 2150  
AGGCCGTGGTGGAGACAGTGGACAATCTGCTCCGGCCAGAAGCTCTGGAG 2200  
TCCTGGAAGGACATGAATGCCACGGAGCAGGTGCACACGGCCACCATGCT 2250  
CCTCGACGTCCTGGAGGAGGGCGCCTTCTGCTGGCCGACAATGTCAGGG 2300  
AGCCTGCCCGCTTCTGGCTGCCAAGGAGAACGTGGTCTGGAGGTCACA 2350  
GTCCTGAACACAGAGGGGCCAGGTGCAGGAGCTGGTGTTCCCCCAGGAGGA 2400  
GTACCCGAGAAAGAACTCCATCCAGCTGTCTGCCAAAACCATCAAGCAGA 2450  
ACAGCCGCAATGGGGTGGTCAAAGTTGTCTTCATCCTCTACAACAACCTG 2500  
GGCCTCTTCTGTCCACGGAGAATGCCACAGTGAAGCTGGCCGGCGAAGC 2550  
AGGCCCGGGTGGCCCTGGGGGCGCCTCTCTAGTGGTGAACCTCACAGGTCA 2600  
TCGCAGCATCCATCAACAAGGAGTCCAGCCGCGTCTTCTCATGGACCCT 2650  
GTCATCTTCACCGTGGCCACCTGGAGGACAAGAACCACTTCAATGCTAA 2700  
CTGCTCCTTCTGGAAGTACTCGGAGCGTTCCATGCTGGGCTATTGGTCCA 2750  
CCCAAGGCTGCCGCCTGGTGGAGTCCAACAAGACCCATACCACGTGTGCC 2800  
TGCAGCCACCTACCAACTTCGCTGTGCTCATGGCTCACCGTGAGATCTA 2850  
CCAGGGCCGCATCAACGAGCTGCTGCTGTGGTGCATCACCTGGGTGGGCA 2900  
TTGTGATCTCCCTGGTCTGCTTGGCCATCTGCATCTCCACCTTCTGCTTC 2950  
CTGCGGGGGCTGCAGACCGACCGCAACACCATCCACAAGAACCTGTGCAT 3000  
CAACCTCTTCTGGCTGAGCTGCTCTTCTGGTGGGATCGACAAGACTC 3050  
AGTATGAGATTGCCTGCCCCATCTTCGCCGGCCTGCTGCACTATTTCTTC 3100  
CTGGCTGCCTTCTCCTGGCTGTGCCTGGAGGGCGTGCACCTCTACCTGCT 3150  
ACTAGTGGAGGTGTTTGAGAGCGAGTATTCCCGCACCAAGTACTACTACC 3200  
TGGGTGGCTACTGCTTCCCGGCCCTGGTGGTGGGCATCGCGGCTGCCATT 3250  
GACTACCGCAGCTACGGCACCGAGAAGGCCTGCTGGCTCCGAGTGGACAA 3300  
TTACTTCATCTGGAGTTTCATCGGGCCAGTCTCCTTCGTTATCGTGGTCA 3350  
ACCTGGTGTTCTCATGGTGACCCTGCACAAGATGATCCGAAGCTCATCT 3400  
GTGCTCAAGCCCGACTCCAGCCGCCTGGACAACATTAAATCCTGGGCGCT 3450  
GGGGGCCATCGCGCTGCTGTTCTGCTGGGCCTCACCTGGGCTTTCGGCC 3500

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Figure 23

TCCTCTTCATCAACAAGGAGTCGGTGGTCATGGCCTATCTCTTCACCACC 3550  
TTCAACGCCTTCCAGGGGGTCTTCATCTTCGTCTTTCACTGCGCCTTACA 3600  
GAAGAAGGTGCACAAGGAGTACAGCAAGTGCCTGCGTCACTCCTACTGCT 3650  
GCATCCGCTCCCCACCCGGGGGCACTCACGGATCCCTCAAGACCTCAGCC 3700  
ATGCGAAGCAACACCCGCTACTACACAGGGACCCAGAGCCGAATTTCGGAG 3750  
GATGTGGAATGACACTGTGAGGAAACAGACGGAGTCCTCCTTCATGGCGG 3800  
GTGACATCAACAGCACCCCCACCCTGAACCGAGGTACCATGGGGAACCAC 3850  
CTGCTGACCAACCCCGTGCTGCAGCCCCGTGGGGGCACCAGTCCCTACAA 3900  
CACCTCATCGCCGAGTCAGTGGGCTTCAATCCCTCCTCGCCCCCTGTCT 3950  
TCAACTCCCCAGGGAGCTACCGGGAACCCAAGCACCCCTTGGGAGGCCGG 4000  
GAAGCCTGTGGCATGGACACCCTGCCCCTGAACGGCAACTTCAATAACAG 4050  
TACTCCTTGCGAAGTGGGGATTTCCCTCCCGGGGATGGGGGCCCTGAGC 4100  
CGCCCCGAGGCCGGAACCTAGCCGATGGGGCGGCCTTTGAGAAGATGATC 4150  
ATCTCAGAGCTGGTGCACAACAACCTGCGGGGGAGCAGCAGCGCGGCCAA 4200  
GGGCCCTCCACCGCCTGAGCCCCCTGTGCCACCTGTGCCAGGGGGCGGGG 4250  
GCGAGGAAGAGGCGGGCGGGCCCCGGGGGTGCTGACCGGGCCGAGATTGAA 4300  
CTTCTCTATAAGGCCCTGGAGGAGCCTCTGCTGCTGCCCCGGGCCAGTC 4350  
GGTGCTGTACCAGAGCGATCTGGACGAGTCGGAGAGCTGCACGGCCGAGG 4400  
ACGGCGCCACCAGCCGGCCCCCTCTCCTCCCTCCTGGCCGGGACTCCCTC 4450  
TATGCCAGCGGGGCCAACCTGCGGGACTCACCTCCTACCCGGACAGCAG 4500  
CCCTGAGGGGCCAGTGAGGCCCTGCCCCACCCCTCCCGCACCCCCCG 4550  
GCCCCCCCCGAAATCTACTACACCTCGCGCCCGCCAGCCCTGGTGGCCCGG 4600  
AATCCCCTGCAGGGCTACTACCAGGTGCGGCGTCCTAGCCACGAGGGCTA 4650  
CCTGGCAGCCCCAGGCCCTTGGGGGCCAGGGCCCGATGGGGACGGGCAGA 4700  
TGCAGCTGGTCACCAGTCTCTGAGGGCACCTCATGGACCAGGGGCTGGTG 4750  
GCCCAGGCCAGGGAGGGAACCTGGGCAGGGCTCTGGTGGGAGAGGGAGA 4800  
CAGATGGAGGCAGTGGCTGGTGGGCCACTCTCTCCAGGTGCCCCCTCAGCC 4850  
ATGGGCCCTACAGTCCCCTCAGGGGACTCTAACCTGGGGGCCTGAGGTGC 4900  
CAGGGTTCACAGACAGGGTTTCCCACCAGCCACACGCACCAGCTCTATTT 4950  
GGGGGAAGTGTAGTGAGGAGGAGCCAGAGGACCCAGGGGAGTGAGGAG 5000  
GGAGAACTTGGAAGGGTGCAGCCCACTTCCAGACTCTCCCCTCTCCACC 5050  
CTTCTACCTGTGAAGGGAAATGAGGGCTTTAGTTTCCTGGGCAGGGAGG 5100  
GGCAGCTTCTGAGGTTGCCAAAGGCCCCCACTGGATGGAACCTGTTAGCT 5150  
GCTCCTCTCCGCAGCCAGAAATGCTGCCGGCTGCACCCAGAGGGAGCAGT 5200  
GAGGCAGGACAGATGGACAGGTTCTCCTGCGCTGTAATTCCTGCTCCC 5250

Figure 24

TGGAGACTGGGAAAAGGCCGCAGGGCAGGGGGACTGGGCGGTGGTGGCTG	5300
GTGGTTTAAAGGTTGAACTTTCTCTGAAGCTCCTTTCCCTTGCTCTTGG	5350
TCCCTGCCCCGCAAGCAAACCTGCCCCCTCTGCCTCCCAGTGCACCCAAT	5400
GACCCCTCCCTTGGGGCGACTCCTGATGAAGCACAACCTCCCCGCAGGGC	5450
CCCAGCCCCACAGGGGTGGCCATATTTGGGCAGTTCCCAGTCCTGTGGGC	5500
TCGGCTATCTGGGGAGCAGATTTTGGGTCTGGATCTCCCTGGGGAGTGGG	5550
TCCTGGGCTTGGATCTTCCCTAGGGGGCCCTCTTACTCCTTCCTCTCTC	5600
CTCCTCCTTCCCCATTGCTGTAAATATTTCAACGAAATGGAAAAGAAAAA	5650
AAAAAAGAC	5659

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Figure 25

